## IN THE SEQUENCE LISTING

Please **replace** the Sequence Listing of record with the Substitute Sequence Listing attached hereto.

NY02:485582.1

## SEQUENCE LISTING

110> MENE-SAFFRANE, Laurent
ESQUERRE-TUGAYE, Marie-Thérèse
FOURNIER, Joëlle
BEFFA, Roland
GROSJEAN-COURNOYER Marie-Claire

<120> LIPOXYGENASE OVEREXPRESSION IN PLANTS AND REDUCTION IN PLANT SENSITIVITY TO DISEASES AND TO ATTACKS FROM PATHOGENIC ORGANISMS

<130> A36097-PCT-USA-A 075188.0117

<140> US/10/731,642

<141> 2003-12-08

<150> PCT/FR02/01943

<151> 2002-06-06

<150> FR 01/07470

<151> 2001-06-07

<150> FR 01/14358

<151> 2001-11-07

<160> 6

<170> Custom

<210> 1

<211> 862

<212> PRT

<213> Nicotiana tabacum

<300>

<308> X84040

<309> 1995-07-16

<400> 1

Met Phe Leu Glu Lys Ile Val Asp Ala Ile Thr Gly Lys Asp Asp Gly
1 5 10 15

Lys Lys Val Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu Asp 20 25 30

Phe Thr Asp Ile Asn Ala Ser Val Leu Asp Gly Val Leu Glu Phe Leu 35 40 45

Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp Pro 50 55 60

Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu Asn 65 70 75 80

Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe Arg

Val	Thr	Phe	Asp 100	Trp	Asp	Asp	Glu	Glu 105	Phe	Gly	Val	Pro	Gly 110	Ala	Phe
Ile	Ile	Lys 115	Asn	Leu	His	Phe	Ser 120	Glu	Phe	Phe	Leu	Lys 125	Ser	Leu	Thr
Leu	Glu 130	Asp	Val	Pro	Asn	His 135	Gly	Lys	Val	His	Phe 140	Val	Cys	Asn	Ser
Trp 145	Val	Tyr	Pro	Ala	Asn 150	Lys	Tyr	Lys	Ser	Asp 155	Arg	Ile	Phe	Phe	Ala 160
Asn	Gln	Ala	Tyr	Leu 165	Pro	Ser	Glu	Thr	Pro 170	Asp	Thr	Leu	Arg	Lys 175	Tyr
Arg	Glu	Asn	Glu 180	Leu	Val	Thr	Leu	Arg 185	Gly	Asp	Gly	Thr	Gly 190	Lys	Leu
Glu	Glu	Trp 195	Asp	Arg	Val	Tyr	Asp 200	Tyr	Ala	Tyr	Tyr	Asn 205	Asp	Leu	Gly
Asp	Pro 210	Asp	Lys	Gly	Gln	Asp 215	Leu	Ser	Arg	Pro	Val 220	Leu	Gly	Gly	Ser
Ser 225	Glu	Tyr	Pro	Tyr	Pro 230	Arg	Arg	Gly	Arg	Thr 235	Gly	Arg	Lys	Pro	Thr 240
Lys	Thr	Asp	Pro	Asn 245	Ser	Glu	Ser	Arg	Ile 250	Pro	Leu	Leu	Met	Ser 255	Let
Asp	Ile	Tyr	Val 260	Pro	Arg	Asp	Glu	Arg 265	Phe	Gly	His	Ile	Lys 270	Leu	Ser
Asp	Phe	Leu 275	Thr	Phe	Ala	Leu	Lys 280	Ser	Ile	Val	Gln	Leu 285	Leu	Leu	Pro
Glu	Phe 290	Lys	Ala	Leu	Phe	Asp 295	Ser	Thr	His	Asn	Glu 300	Phe	Asp	Ser	Phe
Glu 305	Asp	Val	Leu	Lys	Leu 310	Tyr	Glu	Gly	Gly	Ile 315	Lys	Leu	Pro	Gln	Gl <sub>3</sub> 320
Pro	Leu	Leu	Lys	Ala 325	Ile	Thr	Asp	Ser	Ile 330	Pro	Leu	Glu	Ile	Leu 335	Lys
Glu	Leu	Leu	Arg 340	Ser	Asp	Gly	Glu	Gly 345	Leu	Phe	Lys	Tyr	Pro 350	Thr	Pro
Gln	Val	Ile 355	Gln	Glu	Asp	Lys	Thr 360	Ala	Trp	Arg	Thr	Asp 365	Glu	Glu	Phe
Gly	Arg 370	Glu	Met	Leu	Ala	Gly 375	Val	Asn	Pro	Val	Ile 380	Ile	Ser	Arg	Lei
Gla	Clu	Phe	Pro	Pro	T.379	Ser	LVS	Len	Asn	Pro	Lvs	Ile	Tvr	Glv	Asr

Gln Asn Ser Thr Ile Thr Arg Glu Gln Ile Glu Asp Lys Leu Asp Gly 405 410 415

Leu Thr Ile Asp Glu Ala Ile Lys Thr Asn Arg Leu Phe Ile Leu Asn 420 425 430

His His Asp Ile Leu Met Pro Tyr Leu Arg Arg Ile Asn Thr Ser Thr 435 440 445

Asp Thr Lys Thr Tyr Ala Ser Arg Thr Leu Leu Phe Leu Gln Asp Asn 450 455 460

Gly Thr Leu Lys Pro Ser Ala Ile Glu Leu Ser Leu Pro His Pro Asp 465 470 475 480

Gly Asp Gln Phe Gly Ala Val Ser Lys Val Tyr Thr Pro Ala Asp Gln 485 490 495

Gly Val Glu Gly Ser Ile Trp Gln Leu Ala Lys Ala Tyr Ala Ala Val 500 505 510

Asn Asp Ser Gly Val His Gln Leu Ile Ser His Trp Leu Asn Thr His 515 520 525

Ala Ala Ile Glu Pro Phe Val Ile Ala Thr Asn Arg Gln Leu Ser Ala 530 540

Leu His Pro Ile Tyr Lys Leu Leu His Pro His Phe Arg Glu Thr Met 545 550 555 560

Asn Ile Asn Ala Leu Ala Arg Gln Ile Leu Ile Asn Gly Gly Leu
565 570 575

Leu Glu Leu Thr Val Phe Pro Ala Lys Tyr Ser Met Glu Met Ser Ala 580 585 590

Val Val Tyr Lys Asp Trp Val Phe Pro Glu Gln Ala Leu Pro Thr Asp 595 600 605

Leu Ile Lys Arg Gly Val Ala Val Glu Asp Ser Ser Ser Pro Leu Gly 610 620

Ile Arg Leu Leu Ile Gln Asp Tyr Pro Tyr Ala Val Asp Gly Leu Lys 625 630 635 640

Ile Trp Ser Ala Ile Lys Ser Trp Val Thr Glu Tyr Cys Asn Tyr Tyr 645 650 655

Tyr Lys Ser Asp Asp Ala Val Gln Lys Asp Thr Glu Leu Gln Ala Trp
660 665 670

Trp Lys Glu Leu Arg Glu Glu Gly His Gly Asp Lys Lys Asp Glu Pro 675 680 685

Trp Trp Pro Lys Met Gln Thr Val Gln Glu Leu Ile Asp Ser Cys Thr

690 695 700

Ile Thr Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly 705 710 715 720

Gln Tyr Pro Tyr Ala Gly Tyr Leu Pro Asn Arg Pro Thr Leu Ser Arg
725 730 735

Asn Phe Met Pro Glu Pro Gly Ser Pro Glu Tyr Glu Glu Leu Lys Thr 740 745 750

Asn Pro Asp Lys Val Phe Leu Lys Thr Ile Thr Pro Gln Leu Gln Thr 755 760 765

Leu Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Arg His Ser Ser Asp 770 775 780

Thr Leu Tyr Leu Gly Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp Gln 785 790 795 800

Glu Pro Leu Ser Ala Phe Ala Arg Phe Gly Lys Lys Leu Ser Asp Ile 805 810 815

Glu Asp Gln Ile Met Gln Met Asn Val Asp Glu Lys Trp Lys Asn Arg 820 825 830

Ser Gly Pro Val Lys Val Pro Tyr Thr Leu Leu Phe Pro Thr Ser Glu 835 840 845

Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile 850 855 860

<210> 2

<211> 3390

<212> DNA

<213> Artificial sequence

<220>

<223> construct CaMV 35S-LOX

<220>

<221> promoter

<222> (1)..(532)

<223> CaMV 35S promoter

<220>

<221> CDS

<222> (543)..(3131)

<223> Tobacco LOX1 coding sequence

<220>

<221> terminator

<222> (3138)..(3390)

<223> Nos terminator

<400> 2

ccatggagtc aaagattcaa atagaggacc taacagaact cgccgtaaag actggcgaac 60 agttcataca gagtctctta cgactcaatg acaagaagaa aatcttcgtc aacatggtgg 120 agcacgacac gcttgtctac tccaaaaata tcaaagatac agtctcagaa gaccaaaggg 180 caattgagac ttttcaacaa agggtaatat ccggaaacct cctcggattc cattgcccag 240 ctatctqtca ctttattqtq aaqataqtqq aaaaqqaaqq tqqctcctac aaatqccatc 300 attgcgataa aggaaaggcc atcgttgaag atgcctctgc cgacagtggt cccaaagatg 360 gacccccacc cacgaggagc atcgtggaaa aagaagacct tccaaccacg tcttcaaagc 420 aagtggattg atgtgatatc tccactgacg taagggatga cgcacaatcc cactatcctt 480 cqcaaqaccc ttcctcctat aaggaagttc atttcatttg gagaggacac gcggtaccca 540 aa atg ttt ctg gag aag att gtg gat gca atc aca ggg aaa gat gat 587 Met Phe Leu Glu Lys Ile Val Asp Ala Ile Thr Gly Lys Asp Asp 635 gga aaa aag gta aaa gga aca gtg gtt ttg atg aag aaa aat gtt ttg Gly Lys Lys Val Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu gat ttt act gat att aat gcc tca gtt ctt gat gga gtt ctt gag ttc 683 Asp Phe Thr Asp Ile Asn Ala Ser Val Leu Asp Gly Val Leu Glu Phe 35 ctt ggt cgg agg gtc tct ctc gag ttg atc agt tct gtt aat gct gat 731 Leu Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp 50 55 779 cct gca aat ggt tta caa ggg aaa cgc agc aaa gca gca tat ttg gag Pro Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu 65 aac tgg cta aca aat agc acc cca ata gca ggt gaa tca gca ttt 827 Asn Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe 80 aga gtc aca ttt gat tgg gat gat gag gaa ttt gga gtt cca gga gca 875 Arg Val Thr Phe Asp Trp Asp Asp Glu Glu Phe Gly Val Pro Gly Ala 105 110 100 ttc att atc aag aac ttg cat ttt agt gag ttc ttc ctc aag tca ctc 923 Phe Ile Ile Lys Asn Leu His Phe Ser Glu Phe Phe Leu Lys Ser Leu 115 120 971 acc ctt gaa gat gtt cct aat cat ggc aaa gtt cat ttt gtc tgt aat Thr Leu Glu Asp Val Pro Asn His Gly Lys Val His Phe Val Cys Asn 130 tct tgg gtt tat cct gct aat aaa tat aag tca gat cgc atc ttc ttc 1019 Ser Trp Val Tyr Pro Ala Asn Lys Tyr Lys Ser Asp Arg Ile Phe Phe 155 145 150

gcg Ala 160	aat Asn	cag Gln	gct Ala	tat Tyr	cta Leu 165	cca Pro	agt Ser	gaa Glu	aca Thr	cca Pro 170	gac Asp	aca Thr	ttg Leu	cga Arg	aaa Lys 175	1067
					tta Leu											1115
					aga Arg											1163
					ggc Gly											1211
					tat Tyr											1259
					aat Asn 245											1307
					cca. Pro											1355
					ttt Phe											1403
cct Pro	gag Glu	ttt Phe 290	aag Lys	gct Ala	ttg Leu	ttc Phe	gat Asp 295	agc Ser	acg Thr	cat His	aat Asn	gag Glu 300	ttt Phe	gat Asp	agt Ser	1451
					aaa Lys											1499
					gcc Ala 325											1547
					agt Ser											1595
					gag Glu											1643
					ttg Leu											1691

						aaa Lys 390										1739
						acc Thr										1787
						gca Ala										1835
						atg Met										1883
						gcc Ala										1931
						tca Ser 470										1979
						gct Ala										2027
						atc Ile										2075
						cat His										2123
						ttc Phe										2171
						aag Lys 550										2219
						gca Ala										2267
						ttt Phe										2315
						tgg Trp										2363
gat	ctc	atc	aaa	aga	gga	gta	gct	gtt	gag	gac	tcg	agc	tcc	сса	ctt	2411

Asp	Leu	Ile 610	Lys	Arg	Gly	Val	Ala 615	Val	Glu	Asp	Ser	Ser 620	Ser	Pro	Leu		
					att Ile											2459	
					att Ile 645											2507	
					gat Asp											2555	
					cgc Arg											2603	
					atg Met											2651	
					ata Ile	_		_			_					2699 .	
					gct Ala 725											2747	
					gag Glu											2795	
					gta Val											2843	
					tcc Ser										tcg Ser	2891	
					ggg Gly											2939	
					gct Ala 805											2987	
					atg Met											3035	
					aaa Lys											3083	

835 840 845

gaa gga gga ctt act ggc aaa gga att cct aac agt gtg tca ata tag 3131 Glu Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile 855 aactttcccg atctagtaac atagatgaca ccgcgcgcga taatttatcc tagtttgcgc 3191 gctatatttt gttttctatc gcgtattaaa tgtataattg cgggactcta atcataaaaa 3251 cccatctcat aaataacgtc atgcattaca tgttaattat tacatgctta acgtaattca 3311 acagaaatta tatgataatc atcgcaagac cggcaacagg attcaatctt aagaaacttt 3371 3390 attgccaaat gtttgaacg <210> 3 <211> 30 <212> DNA <213> Artificial sequence <220> <223> Artificial sequence description: Sense primer <400> 3 30 gttatcaaac agtttaaaat gtttctggag <210> 4 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Artificial sequence description: Reverse primer <400> 4 22 tgatttaaag ttctatattg ac <210> 5 <211> 20 <212> DNA <213> Artificial sequence <220> <223> Artificial sequence description: Primer F <400> 5 20 ggccatggag tcaaagattc <210> 6

<211> 19

```
<212> DNA
<213> Artificial sequence
<220>
<223> Artificial sequence description: Primer R
<400> 6
gctctggcat gaaatttcg
```